NUCLEIC SEQUENCES CODING FOR AN AT2
Inventor(s): Elbaz, et al.
Application No: 09/762,194
Atty Dkt No: 33339/208804

09/762194

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LOCUS   AT2 receptor C-terminal end   160 BP DS-DNA

ORGANISM   Mouse
BASES   41 A   33 C   36 G   50 T

Nucleic acids 1 TGTGTTAATC CCTTCCTGTA TTGTTTTGTT GGAAACCGCT
                 TCCAACAGAA CGTCCGCAGT GTGTTTAGAG TTCCCATTAC
                 TTGGCTCCAA GGCAAGAGAG AGACTATGTC TTGCAGAAAA
             121 GGCAGTTCTC TTAGAGAAAT GGACACCTTT GTGTCTTAAA

Translation into amino acids

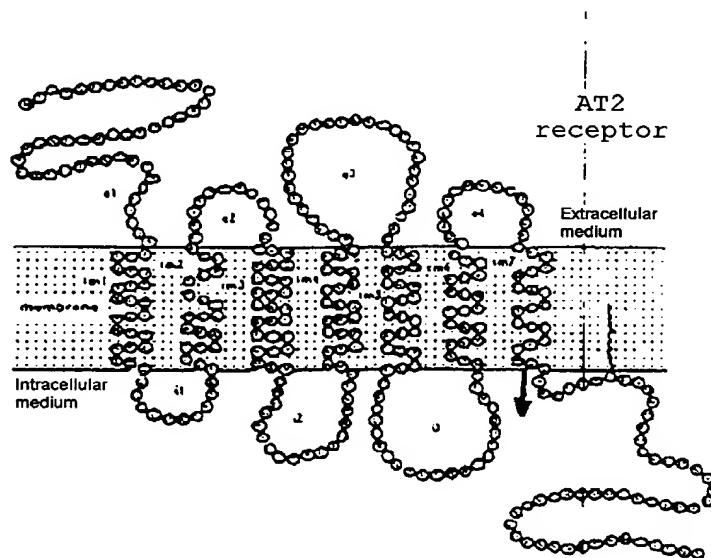   CVNPFLYCFV GNRFQQNVRS VFRVPITWLQ GKRETMSCRK
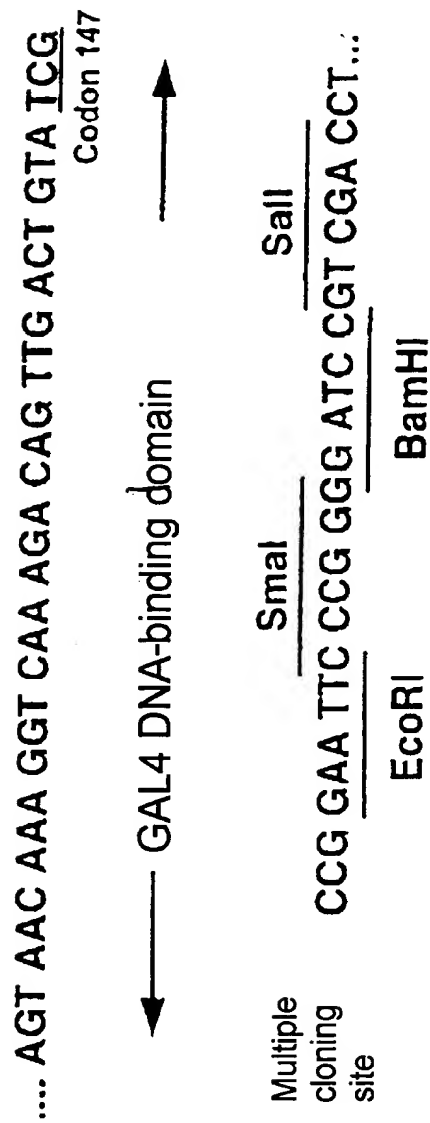   GSSLREMDTFVS·

Figure 1

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... AGT AAC AAA GGT CAA AGA CAG TTG ACT GTA <u>TCG</u>
Codon 147

⟶ GAL4 DNA-binding domain

Multiple
cloning
site

EcoRI   <u>Smal</u>   <u>Sall</u>
CCG GAA TTC CCG GGG ATC CGT CGA CCT...
<u>BamHI</u>

<u>Figure 2</u>

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GCTACCCCCCCCCCACGCACCCCCCAATCTGGGTGCCCTGGCATTAGCATGTAAGCTTGTTTTTCTCTGGC        71

TGTATCTCTTGGCCTGGAAGAACCCCGAGTTGCCAAGAGACACAGTATGTGATGGTCCCTGGAAAAGCTGCT      143

                              M   L   L   S   P   R   F   S   L        9
TCCCTGCGAAGTTCTCCCACTGCCTTCGAAGAC ATG CTG TTG TCT CCC AAA TTC TCC TTA        204

    S   T   I   H   V   R   L   T   A   K   G   L   L   R   N   L   R   L     27
    TCC ACC ATC CAC GTC CGC CTA ACC GCC AAA GGA CTG CTT CGA AAC CTC CGG CTT    258

    P   S   G   L   R   K   N   T   V   I   F   H   T   V   E   K   G   R     45
    CCT TCG GGG CTC AGG AAA AAC ACT GTC ATT TTC CAC ACA GTT GAA AAG GGC AGG    312

    Q   K   N   P   R   S   L   C   I   Q   T   Q   T   A   P   D   V   L     53
    CAG AAG AAT CCC AGG AGC CTG TGC ATC CAG ACC CAG ACA GCT CCA GAT GTG CTG    366

    S   S   E   R   T   L   E   L   A   Q   Y   K   T   K   C   E   S   Q     81
    TCC TCC GAG AGA ACG CTT GAG TTG GCC CAA TAC AAG ACA AAA TGT GAA AGC CAA    420

    S   G   F   I   L   H   L   R   Q   L   L   S   R   G   N   N   K   F     99
    AGT GGA TTC ATC CTG CAC CTC AGG CAG CTT CTT TCC CGT GGT AAC AAC AAG TTT    474

    E   A   L   T   V   V   I   Q   H   L   L   S   E   R   E   E   A   L     117
    GAA GCG CTG ACA GTT GTG ATC CAG CAC CTC CTG TCT GAG CGG GAG GAA GCA CTG    528

    K   Q   H   K   T   L   S   Q   E   L   V   S   L   R   G   E   L   V     135
    AAG CAA CAC AAA ACC CTC TCT CAA GAA CTT GTC AGC CTC CGG GGA GAG CTA GTT    582

 1  A   A   S   S   A   C   E   K   L   E   K   A   R   A   D   L   Q   T     153
    GCT GCT TCA AGC GCC TGT GAG AAG CTA GAA AAG GCT AGG GCT GAC TTA CAG ACA    636

    A   Y   Q   E   F   V   Q   K   L   N   Q   Q   H   Q   T   D   R   T     171
    GCG TAT CAA GAA TTT GTC CAG AAA CTA AAC CAG CAG CAT CAG ACA GAC CGG ACG    690

    E   L   E   N   R   L   K   D   L   Y   T   A   E   C   E   K   L   Q     189
    GAA CTG GAG AAC CGG CTG AAG GAC TTA TAC ACC GCA GAG TGT GAG AAG CTT CAG    744

    S   I   Y   I   E   E   A   E   K   Y   K   T   Q   L   Q   E   Q   F     207
    AGC ATT TAC ATT GAG GAG GCA GAA AAA TAT AAA ACT CAA CTG CAA GAG CAG TTT    798

 2  D   N   L   N   A   A   H   E   T   T   K   L   E   I   E   A   S   H     225
    GAC AAC TTA AAC GCC GCC CAT GAG ACC ACT AAG CTT GAG ATT GAA GCT AGC CAC    852

    S   E   K   V   E   L   L   K   K   T   Y   E   T   S   L   S   E   I     243
    TCG GAG AAG GTG GAA TTG CTG AAG AAG ACC TAT GAA ACC TCT CTT TCA GAA ATC    906

    K   K   S   H   E   M   E   K   K   S   L   E   D   L   L   N   E   K     261
    AAG AAG AGC CAT GAG ATG GAG AAG AAG TCA CTG GAG GAT CTG CTT AAT GAG AAG    960

    Q   E   S   L   E   K   Q   I   N   D   L   K   S   E   N   D   A   L     279
    CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG AAG AGT GAA AAC GAT GCT TTA   1014

 3  N   E   R   L   K   S   E   E   Q   K   Q   L   S   R   E   K   A   N     297
    AAC GAA AGG TTG AAA TCA GAG GAG CAA AAG CAA CTG TCA AGA GAG AAG GCG AAT   1068

    S   K   N   P   Q   V   M   Y   L   E   Q   E   L   E   S   L   K   A     315
    TCC AAA AAC CCT CAG CTC ATG TAT CTG GAG CAA GAA CTA GAA AGC CTG AAG CCT   1122
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Figure 3.1

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  V   L   E   I   K   N   E   K   L   H   Q   Q   D  |M   K   L   M   K    333
GTG TTA GAG ATC AAG AAT GAG AAG CTG CAC CAG CAG GAC|ATG AAG CTA ATG AAG   1176
_____
  M   E   K   L   V   D   N   N   T   A   L   V   D  ,K   L   K   R   F    351
ATG GAA AAG CTG GTG GAC AAT AAC ACA GCA TTG GTT GAC|AAG CTG AAG CGA TTC   1230
_____
  Q   Q   E   N   E   S   L   K   A   R   M   D   K  |H   M   A   I   S    369
CAG CAG GAA AAC GAG GAG TTA AAA GCT CGC ATG GAC AAA|CAC ATG GCA ATT TCA   1296
_____
  R   Q   L   S   T   E   Q   A   A   L   Q   E   S  |L   E   K   E   S    387
AGG CAA CTT TCC ACC GAG CAG GCC GCG CTG CAA GAG TCC|CTT GAG AAG GAG TCA   1338
_____
  K   V   N   K   R   L   S   M   E   N   E   E   L  |L   W   K   L   H    405
AAG GTC AAC AAG AGA CTG TCC ATG GAG AAC GAG GAA CTT|CTG TGG AAA CTG CAC   1392
_____
  N   G   D   L   C   S   P   K   R   S   P   T   S  |S   A   I   P   F    423
AAC GGA GAC CTG TGC AGC CCC AAG AGA TCC CCC ACC TCC|TCG GCC ATC CCT TTC   1446
_____
  Q   S   P   R   N   S   G   S   F   S   S   P   S  |I   S   P   R   *    440
CAG TCC CCC AGG AAT TCT GGT TCC TTC TCC AGC CCC AGC|ATC TCA CCC AGA TGA   1500

CGGCTTCTGAACGCAGGAGACTCTCTGAAGGCACTGAGGTGCGCTTCTGCAGGACTGACCCTCTCATGGGA   1571

ACTCGAGTTGCTGCGTTAGCTCTCTGGAATATCCCCAGGATATCGGGAGAGCAGCCGCCAACCGTATCAGC   1643

TACGTACGAATAGAGAGCTCCAATAGAAGACTTTTAACTTGGTCCAAAAGCCTCCTCCAAAAACAGATTTC   1713

GGAACTGAAGTGGACATAGTTGCACAAAGCACTTACGGAACGAGGGAACCTTGTTCTTTGCCTTCCTTCAC   1784

CTAAGCATAGGCTTTCCAG                                                        1803
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Figure 3₂

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cagtgtgatgtggttcagaggcagcttctagaccttgcaggagggagattgtattcagaggaagagcaccatt    72

ttggcaacatctgaaagtgaaaacggaagccagaaacacttggccagccctgggggatttttttcttcctatg    144

cccctgtggctgaatgacatttgctgtcgtaggcatctttcctctgactgtatttcttggcttcgaagagtac    215

tgagcttaaaaagacagtatgctgacagtccatggaaattgccccctcctgtgaaatttcgccacctgctccgt    288

agac ATG TTG TTG TCT CCC AAA TTC TCC TTA TCC ACC ATT CAC ATA CGA CTG ACG    343
      M   L   L   S   P   K   F   S   L   S   T   I   H   I   R   L   T     17

GCC AAA GGA TTG CTT CGA AAC CTT CGA CTT CCT TCA GGG TTT AGG AGA AGC ACT    397
 A   K   G   L   L   R   N   L   R   L   P   S   G   F   R   R   S   T     35

GTT GTT TTC CAC ACA GTT GAA AAG AGC AGG CAA AAG AAT CCT CGA AGC TTA TGT    451
 V   V   F   H   T   V   E   K   S   R   Q   K   N   P   R   S   L   C     53

ATC CAG CCA CAG ACA GCT CCC GAT GCG CTG CCC CCT GAG AAA ACA CTT GAA TTG    505
 I   Q   P   Q   T   A   P   D   A   L   P   P   E   K   T   L   E   L     71

ACG CAA TAT AAA ACA AAA TGT GAA AAC CAA AGT GGA TTT ATC CTG CAG CTC AAG    559
 T   Q   Y   K   T   K   C   E   N   Q   S   G   F   I   L   Q   L   K     89

CAG CTT CTT GCC TGT GGT AAT ACC AAG TTT GAG GCA TTG ACA GTT GTG ATT CAG    613
 Q   L   L   A   C   G   N   T   K   F   E   A   L   T   V   V   I   Q     107

CAC CTG CTG TCT GAG CGG GAG GAA GCA CTG AAA CAA CAC AAA ACC CTA TCT CAA    667
 H   L   L   S   E   R   E   E   A   L   K   Q   H   K   T   L   S   Q     125

GAA CTT GTT AAC CTC CGG GGA GAG CTA GTC ACT GCT TCA ACC ACC TGT GAG AAA    721
 E   L   V   N   L   R   G   E   L   V   T   A   S   T   T   C   E   K     143

TTA GAA AAA GCC AGG AAT GAG TTA CAA ACA GTG TAT GAA GCA TTC GTC CAG CAG    775
 L   E   K   A   R   N   E   L   Q   T   V   Y   E   A   F   V   Q   Q     161

CAC CAG GCT GAA AAA ACA GAA CGA GAG AAT CGG CTT AAA GAG TTT TAC ACC AGG    829
 H   Q   A   E   K   T   E   R   E   N   R   L   K   E   F   Y   T   R     179

GAG TAT GAA AAG CTT CGG GAC ACT TAC ATT GAA GAA GCA GAG AAG TAC AAA ATG    883
 E   Y   E   K   L   R   D   T   Y   I   E   E   A   E   K   Y   K   M     197

CAA TTG CAA GAG CAG TTT GAC AAC TTA AAT GCG CAT GAA ACC TCT AAG TTG GAA    937
 Q   L   Q   E   Q   F   D   N   L   N   A   H   E   T   S   K   L   E     215

ATT GAA GCT AGC CAC TCA GAG AAA CTT GAA TTG CTA AAG AAG GCC TAT GAA GCC    991
 I   E   A   S   H   S   E   K   L   E   L   L   K   K   A   Y   E   A     233

TCC CTT TCA GAA ATT AAG AAA GGC CAT GAA ATA GAA AAG AAA TCG CTT GAA GAT    1045
 S   L   S   E   I   K   K   G   H   E   I   E   K   K   S   L   E   D     251

TTA CTT TCT GAG AAG CAG GAA TCG CTA GAG AAG CAA ATC AAT GAT CTG AAG AGT    1099
 L   L   S   E   K   Q   E   S   L   E   K   Q   I   N   D   L   K   S     269

GAA AAT GAT GCT TTA AAT GAA AAA TTG AAA TCA GAA GAA CAA AAA AGA AGA GCA    1153
 E   N   D   A   L   N   E   K   L   K   S   E   E   Q   K   R   R   A     287

AGA GAA AAA GCA AAT TTG AAA AAT CCT CAG ATC ATG TAT CTA GAA CAG GAG TTA    1207
 R   E   K   A   N   L   K   N   P   Q   I   M   Y   L   E   Q   E   L     305
```

Figure 4

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GAA AGC CTG AAA GCT GTC TTA GAG ATC AAG AAT GAG AAA CTG CAT CAA CAG GAC   1261
 E   S   L   K   A   V   L   E   I   K   N   E   K   L   H   Q   Q   D     323

ATC AAG TTA ATG AAA ATG GAC AAA CTG GTG GAC AAC AAC ACA GCA TTG GTT GAC   1315
 I   K   L   M   K   M   D   K   L   V   D   N   N   T   A   L   V   D     341

AAA TTG AAG CGT TTC CAG CAG GAG AAT GAA GAA TTG AAA GCT CGG ATG GAC AAG   1369
 K   L   K   R   F   Q   Q   E   N   E   E   L   K   A   R   M   D   K     359

CAC ATG GCA ATC TCA AGG CAG CTT TCC ACG GAG CAG GCT GTT CTG CAA GAG TCG   1423
 H   M   A   I   S   R   Q   L   S   T   E   Q   A   V   L   Q   E   S     377

CTG GAG AAG GAG TCG AAA GTC AAC AAG CGA CTC TCT ATG GAA AAC GAG GAG CTT   1477
 L   E   K   E   S   K   V   N   K   R   L   S   M   E   N   E   E   L     395

CTG TGG AAA CTG CAC AAT GGG GAC CTG TGT AGC CCC AAG AGA TCC CCC ACA TCC   1531
 L   W   K   L   H   N   G   D   L   C   S   P   K   R   S   P   T   S     413

TCC GCC ATC CCT TTG CAG TCA CCA AGG AAT TCG GGC TCC TTC CCT AGC CCC AGC   1585
 S   A   I   P   L   Q   S   P   R   N   S   G   S   F   P   S   P   S     431

ATT TCA CCC AGA TGA   cacgtccccaaagcccacagactctttgaaagcatcctgatgcaggtctgc   1651
 I   S   P   R   *                                                        436

aggactgaccccaaggaggaccgtgggcacaagaggtatatcagcacacgtgtgatcaccgtaggtoactgg   1723

agcgtcaccaccggcggaatcgagcttctgagactggaagtctggaggaagactcctgcctccgtccaaaag   1795

attcctccaaaaaaagattcaaaaaaagacttcggcatcgacacggacgttgttgcacaaagcacttaaaga   1867

acgagagcatcttgttcattgcctttttccacctaagcataaggggaaaaactctcagggccctactaagatt   1939

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agggagagggtataacaggaagagcttgacttgtccctgtctatacattctctgtatctttgggggtaac   2299

tcctgctcagtttttcagtgttcagccatgtcagttgaaactagattttctgtagatttttcacttaccca   2371

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Figure 4.2

Title: NUCLEIC SEQUENCES CODING FOR AN AT2
Inventor(s): Elbaz, et al.
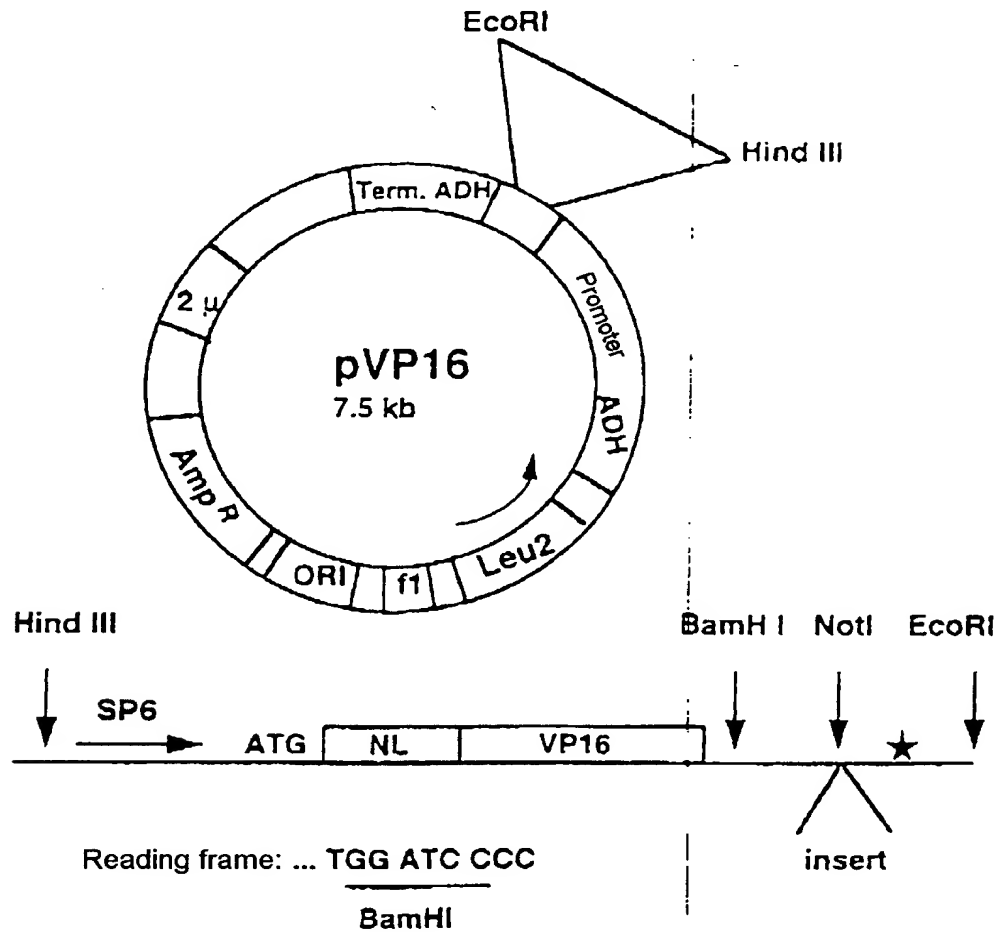Application No: 09/762,194
Atty Dkt No: 33339/208804

09/762194

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tgttcttttaaattagtgattttgtgtcttaagtcttcaacttccaatacttcatcatgtatgtatcctctc  3307

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tgtagaatgcaaaatgttggcacgttaaaaatatgaatgtgtagacaactgtdgttgtgtgctcagtttgtagt  3667

gatgggaagtgtatcttcacttctgatcaaataaataatgctggaatactcaaadaaaaaaaaaaaaaaaaaa  3739

aaa                                                                        3742
```

Figure 4.3

Figure 5

Title: NUCLEIC SEQUENCES CODING FOR AN AT2...
Inventor(s): Elbaz, et al.
Application No: 09/762,194
Atty Dkt No: 33339/208804

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Figure 6

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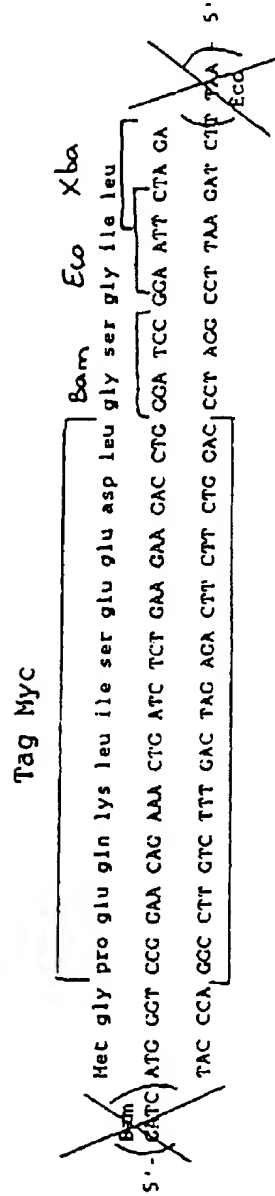
Figure 7

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CHO-hAT2

Lectin column
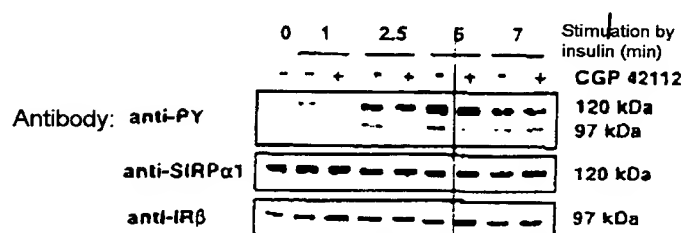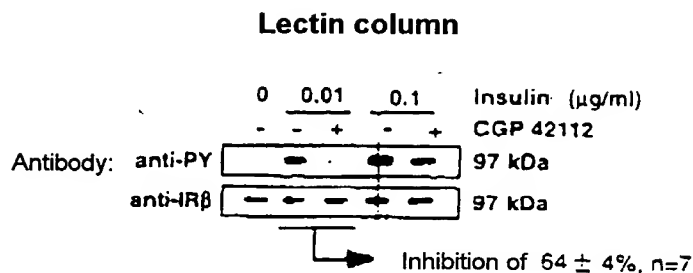
CHO-hAT2 et CHO-hAT2-ATIP

<u>**Figure 11**</u>

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Figure 8

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Tissues:

Pancreas
Kidney
Skeletal muscle
Liver
Lung
Placenta
Brain
Heart

Kb

— 9.5
— 7.5

— 4.4

— 2.4

— 1.3

Figure 9

Figure 10